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14. ABSTRACT The purpose of this study is to evaluate similarities between GWI and known autoimmune disorders. The primary emphasis of the second year of the grant has been continued recruitment of study participants and initial data analysis. We have completed 62 acquisitions during the second year of the grant. In addition, we have published 2 manuscripts supported by this grant. One demonstrated similar brain function in Gulf War Illness and known autoimmune conditions (Georgopoulos et al., 2017); the other demonstrated that a specific Human Leukocyte Antigen allele (DRB1*13:02) protects against brain atrophy in Gulf War veterans (James et al., 2017).					
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## 1. **INTRODUCTION:**

GWII has affected a large number of veterans of the 1990-1991 Persian Gulf War. GWII symptoms are characterized by chronic health problems, of unknown etiology. They resemble symptoms seen in various autoimmune disorders and are reflected in altered patterns of brain function. In this study, we comprehensively assess the association of GWII to autoimmune disorders using cutting-edge measures of brain structure and function, genetic analysis, and laboratory tests. In preliminary studies, we have discovered that GWII possesses a distinct functional brain pattern that is very close to that observed in a well-known autoimmune disorder, Sjogren's syndrome. Hence, the main goal of this proposal is to test the hypothesis that GWII is an autoimmune disorder. For that purpose, we are comparing the results of brain, genetic and laboratory tests in subjects with GWII to those obtained from subjects with known autoimmune disorders, to determine the extent to which GWII reflects autoimmune abnormalities. Altogether, our study will improve knowledge of GWII pathophysiology and ultimately inform diagnosis and potential treatment of GWII, e.g. along lines currently in use for treating autoimmune disorders. It is expected that useful outcomes will be obtained by the end of the 3-year grant period.

2. **KEYWORDS:** Gulf War Illness, autoimmune, neuroimaging, genetics, biomarkers

## 3. **ACCOMPLISHMENTS:**

### ▪ **What were the major goals of the project?**

The major goals of the project are to assess and compare 1) brain structure and function, 2) blood inflammatory and immune markers; 3) HLA genes; and 4) cognitive, mental health, neurological and general standardized clinical status in veterans with Gulf War Illness relative to veterans with autoimmune disorders.

### ▪ **What was accomplished under these goals?**

During this reporting period, we have continued to recruit study participants and have completed an additional 62 acquisitions with many more scheduled in the coming months.

### ▪ **What opportunities for training and professional development has the project provided?**

Nothing to report.

### ▪ **How were the results disseminated to communities of interest?**

We published 2 manuscripts (included as attachments) during this reporting period.

### ▪ **What do you plan to do during the next reporting period to accomplish the goals?**

We plan to continue recruitment, data analysis, and dissemination of study findings.

4. **IMPACT:**

- **What was the impact on the development of the principal discipline(s) of the project?**

Nothing to report.

- **What was the impact on other disciplines?**

Nothing to report.

- **What was the impact on technology transfer?**

Nothing to report.

- **What was the impact on society beyond science and technology?**

Nothing to report.

5. **CHANGES/PROBLEMS:**

- **Changes in approach and reasons for change**

Nothing to report.

- **Actual or anticipated problems or delays and actions or plans to resolve them**

While the project start was delayed due to installation of a new magnetic resonance imaging scanner in the Minneapolis VA's Radiology service, we have accelerated recruitment in the current reporting period to meet study goals.

- **Changes that had a significant impact on expenditures**

Nothing to report.

- **Significant changes in use or care of human subjects, vertebrate animals, biohazards, and/or select agents**

Nothing to report.

- **Significant changes in use or care of human subjects.**

Nothing to report.

- **Significant changes in use or care of vertebrate animals.**

Not applicable.

- **Significant changes in use of biohazards and/or select agents**

Not applicable.

## 6. **PRODUCTS:**

- **Publications, conference papers, and presentations**

### **Journal publications.**

Georgopoulos, A.P., James, L.M., Carpenter, A.F., Engdahl, B.E., Leuthold, A.C., & Lewis, S.M. Gulf War Illness (GWI) as a neuroimmune disease. *Experimental Brain Research*. Epub ahead of print. doi: 10.1007/s00221-017-5050-0

James, L.M., Christova, P., Engdahl, B. E., Lewis, S. M., Carpenter, A. F., & Georgopoulos, A. P. Human Leukocyte Antigen (HLA) and Gulf War Illness (GWI): HLA-DRB1\*13:02 spares subcortical atrophy in Gulf War veterans. *Ebiomedicine* 2017; 26: 126-131. doi: 10.1016/j.ebiom.2017.11.005

- **Books or other non-periodical, one-time publications.**

Nothing to report.

- **Other publications, conference papers, and presentations.**

Nothing to report.

- **Website(s) or other Internet site(s)**

[http://brain.umn.edu/GWI\\_autoimmune.shtml](http://brain.umn.edu/GWI_autoimmune.shtml)

- **Technologies or techniques**

Nothing to report.

- **Inventions, patent applications, and/or licenses**

Nothing to report.

- **Other Products**

We have developed a database in order to facilitate data analysis and dissemination of research findings.

## 7. PARTICIPANTS & OTHER COLLABORATING ORGANIZATIONS

### What individuals have worked on the project?

Name:	<i>Apostolos Georgopoulos</i>
Project Role:	<i>PI</i>
Researcher Identifier (e.g. ORCID ID):	
Nearest person month worked:	<i>2</i>
Contribution to Project:	<i>Study design and oversight.</i>
Funding Support:	<i>VA CSR&amp;D</i>

Name:	<i>Brian Engdahl</i>
Project Role:	<i>Co-Investigator</i>
Researcher Identifier (e.g. ORCID ID):	
Nearest person month worked:	<i>2</i>
Contribution to Project:	<i>Identification of potential participants.</i>
Funding Support:	<i>VA CSR&amp;D</i>

Name:	<i>Lisa James</i>
Project Role:	<i>Co-Investigator</i>
Researcher Identifier (e.g. ORCID ID):	
Nearest person month worked:	<i>3</i>
Contribution to Project:	<i>Completion of regulatory documents, participant recruitment, and data acquisition.</i>
Funding Support:	<i>VA CSR&amp;D</i>

Name:	<i>Arthur Leuthold</i>
Project Role:	
Researcher Identifier (e.g. ORCID ID):	<i>1234567</i>

Nearest person month worked:	2
Contribution to Project:	<i>MEG data acquisition, quality control, and pre-processing.</i>
Funding Support:	VA CSR&D

Name:	<i>Adam Carpenter</i>
Project Role:	Other significant contributor
Researcher Identifier (e.g. ORCID ID):	
Nearest person month worked:	2
Contribution to Project:	<i>Oversight of neurological exams and MRI acquisition.</i>
Funding Support:	

- **Has there been a change in the active other support of the PD/PI(s) or senior/key personnel since the last reporting period?**

A pending grant involving Drs. Georgopoulos, James, Engdahl, and Carpenter has been awarded in this reporting period.

- **What other organizations were involved as partners?**

Nothing to report.

## 8. SPECIAL REPORTING REQUIREMENTS

Nothing to report.

## 9. APPENDICES

The following recently published manuscripts are attached:

Georgopoulos, A.P., James, L.M., Carpenter, A.F., Engdahl, B.E., Leuthold, A.C., & Lewis, S.M. Gulf War Illness (GWI) as a neuroimmune disease. *Experimental Brain Research*. Epub ahead of print.  
doi: 10.1007/s00221-017-5050-0



James, L.M., Christova, P., Engdahl, B. E., Lewis, S. M., Carpenter, A. F., & Georgopoulos, A. P. Human Leukocyte Antigen (HLA) and Gulf War Illness (GWI): HLA-DRB1\*13:02 spares subcortical atrophy in Gulf War veterans. *Ebiomedicine* 2017; 26: 126-131. doi: 10.1016/j.ebiom.2017.11.005



## Research Paper

# Human Leukocyte Antigen (HLA) and Gulf War Illness (GWI): HLA-DRB1\*13:02 Spares Subcortical Atrophy in Gulf War Veterans



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Cerebellum

## ABSTRACT

**Background:** Gulf War Illness (GWI) is a multisystem disorder that has affected a substantial number of veterans who served in the 1990–91 Gulf War. The brain is prominently affected, as manifested by the presence of neurological, cognitive and mood symptoms. We reported previously on the protective role of six Human Leukocyte Antigen (HLA) alleles in GWI (Georgopoulos et al., 2016) and their association with regional brain function (James et al., 2016). More recently, we reported on the presence of subcortical brain atrophy in GWI (Christova et al., 2017) and discussed its possible relation to immune mechanisms. Here we focused on one of the six HLA GWI-protective HLA alleles, DRB1\*13:02, which has been found to have a protective role in a broad range of autoimmune diseases (Furukawa et al., 2017), and tested its effects on brain volumes.

**Methods:** Seventy-six Gulf War veterans (55 with GWI and 21 healthy controls) underwent a structural Magnetic Resonance Imaging (sMRI) scan to measure the volumes of 9 subcortical brain regions to assess differences between participants with (N = 11) and without (N = 65) HLA class II allele DRB1\*13:02.

**Findings:** We found that DRB1\*13:02 spared subcortical brain atrophy in Gulf War veterans; overall subcortical volume was 6.6% higher in carriers of DRB1\*13:02 (P = 0.007). The strongest effect was observed in the volume of cerebellar gray matter which was 9.6% higher (P = 0.007) in carriers of DRB1\*13:02 than in non-carriers. By contrast, DRB1\*13:01 had no effect.

**Interpretation:** These findings document the protective effect of DRB1\*13:02 on brain atrophy in Gulf War veterans and are in keeping with recent results documenting sharing of brain mechanisms between GWI and other immune-related diseases (Georgopoulos et al., 2017). We hypothesize that the protective role of DRB1\*13:02 is due to its successful elimination of external antigens to which Gulf War veterans were exposed, antigens that otherwise would persist causing low-grade inflammation and possibly leading to autoimmunity.

**Funding source:** U.S. Department of Defense (W81XWH-15-1-0520), Department of Veterans Affairs, American Legion Brain Sciences Chair, and University of Minnesota.

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## 1. Introduction

### 1.1. Gulf War Illness

For over 25 years, veterans of the 1990–1991 Gulf War (GW) have been affected by chronic health problems, commonly referred to as Gulf War Illness (GWI), that are presumed to be sequelae of service-

related exposures to toxins such as pyridostigmine bromide, pesticides, multiple vaccinations, and/or stress (White et al., 2016). Many symptoms of GWI involve the central nervous system; consequently, several studies have investigated brain structure and function as it relates to GWI, with mixed findings (White et al., 2016). We have recently identified functional (Engdahl et al., 2016) and structural (Christova et al., 2017) brain anomalies in GWI, both of which prominently involved subcortical regions. For example, compared to healthy control veterans, veterans with GWI showed an average of 10.4% reduction in cerebellar volume and 2× the rate of reduction of cerebellar gray matter volume with age (−14%/decade in GWI vs. −6.9%/decade in controls). We

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concluded that the marked subcortical volume reduction observed in veterans with GWI is likely attributable to direct exposure to toxins, akin to toxic encephalopathy (Valk and van der Knaap, 1992), in combination with lack of immunogenetic protection in GWI (Georgopoulos et al., 2016; James et al., 2016).

### 1.2. Immunogenetics and GWI

Although a quarter to one-third of GW veterans suffer from GWI (Research Advisory Committee on Gulf War Veterans' Illnesses, 2014), most GW veterans remain relatively healthy, suggesting that genetic variations likely play a role in determining their health outcomes. In fact, we have found robust evidence that genetic variations involving the Human Leukocyte Antigen (HLA) play a substantial role in promoting protection against or vulnerability to GWI (Georgopoulos et al., 2016). HLA genes are located in the Major Histocompatibility Complex (MHC) of chromosome 6 and play a central role in immune system functioning (Meuer et al., 1982). We previously demonstrated that six HLA class II alleles (DRB1\*01:01, DRB1\*08:11, DRB1\*13:02, DQB1\*02:02, DPB1\*01:01, DPB1\*06:01) successfully discriminate veterans with GWI from controls (Georgopoulos et al., 2016) and interact with brain function to influence symptoms of GWI (James et al., 2016). We also found an inverse relation between GWI symptom severity and the number of copies of the 6 protective HLA alleles, and that the frequency of those 6 alleles in veterans with GWI is significantly lower than in unaffected veterans (Georgopoulos et al., 2016). These effects suggest that the presence of these HLA alleles confers protection against GWI.

Notably, all 6 of the protective HLA alleles identified in relation to GWI belong to HLA class II alleles. HLA class II alleles have been strongly associated with various immune-related conditions including multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus, celiac disease, Crohn's disease, and Graves' disease, among others (Shiina et al., 2009; Gough and Simmonds, 2007). This overlap, in conjunction with several overlapping clinical signs and symptoms (Israeli, 2012), including similarities in brain synchronicity (Georgopoulos et al., 2017), places GWI squarely within the immune dysfunction realm.

### 1.3. Protective Effects of DRB1\*13:02

Of the six HLA alleles previously identified as protective in terms of GWI (Georgopoulos et al., 2016), DRB1\*13:02 has been found to be protective in various immune-related disorders (Bettencourt et al., 2015; Furukawa et al., 2017). Other HLA alleles have either received relatively minimal investigation in regards to their relation to autoimmune disorders, have been shown to promote susceptibility, or findings are mixed in terms of conferring susceptibility or resistance to various immune-related diseases. In a large study of associations between DRB1 alleles and six autoimmune disorders, DRB1\*13 was found to be a protective factor for four autoimmune disorders (rheumatoid arthritis, systemic lupus erythematosus, psoriasis/psoriatic arthritis, and systemic sclerosis), whereas other DRB1 alleles were risk factors (Bettencourt et al., 2015). HLA DRB1\*03, for instance, was strongly linked to 3 autoimmune disorders (systemic lupus erythematosus, multiple sclerosis, and myasthenia gravis). Thus, it appears that several autoimmune disorders share immunogenetic mechanisms, with DRB1\*13 promoting protection, particularly for systemic and rheumatic diseases. Furthermore, the protective effects appear to be especially robust for the DRB1\*13:02 allele. This protein contains 266 amino acids, of which amino acid residues at positions 30–266 form the beta chain. DRB1\*13:02 contains a glycine residue at chain position 86, and differs by only one residue from the DRB1\*13:01 protein which contains a valine residue at position 86. This single residue substitution makes a large difference in the electrostatic properties of pocket 9 (P9) of the peptide binding groove, i.e. the part of the HLA protein that binds to external antigens (Hov et al., 2011). DRB1\*13:02 has been found to be protective against various

systemic and organ-specific autoimmune disorders with gene-dosage effects conferring maximal protection in homozygous DRB1\*13:02 carriers (for review, see Furukawa et al., 2017). DRB1\*13:01 has also been found to protect against rheumatoid arthritis (van der Woude et al., 2010) but to be a risk factor for protracted hepatitis A infection (Pando et al., 1999) and associated pediatric autoimmune hepatitis (Fainboim et al., 2001), as well as primary sclerosing cholangitis (Hov et al., 2011). These mixed findings show that different alleles (DRB1\*13:01, DRB1\*13:02) can have very different disease associations, such that exploring such relations at the allele level (DRB1\*13) can be misleading and uncertain. These considerations underscore the need to investigate HLA-disease associations at the protein (4-digit resolution) level, as pioneered by Todd et al. (1987) in the case of type 1 diabetes mellitus and further carried out following the publication of the crystal structures of the HLA class II molecule by Brown et al. (1993) (Jones et al., 2006).

### 1.4. The Present Study

Given the reported protective role of DRB1\*13:02 for immune-related diseases and the evidence that GWI is closely related to such disorders (Georgopoulos et al., 2016, 217), we investigated the effect of DRB1\*13:02 on the volumes of subcortical brain regions found to be reduced in GWI (Christova et al., 2017) to test the hypothesis that HLA DRB1\*13:02 prevents subcortical brain atrophy in GW veterans, thus exerting a protective role in GWI too.

## 2. Materials and Methods

### 2.1. Participants

Seventy-six GW-era veterans (55 men, 21 women; mean age  $\pm$  SEM,  $53.87 \pm 1.17$  y) participated in the current study after providing informed consent, in adherence to the Declaration of Helsinki, and were financially compensated for their time. They included 55 veterans with GWI (52 men, 3 women) and 21 healthy controls (3 men, 18 women). All study protocols were approved by the appropriate Institutional Review Boards. GWI status was determined using a self-report symptom checklist that permits classification as GWI case or control according to the Center for Disease Control (Fukuda et al., 1998) and the Kansas criteria (Steele, 2000). All GWI veterans in the present study met both case definitions. Study participants completed diagnostic interviews including the Clinician-Administered PTSD Scale for DSM-IV (Blake et al., 1995) and the Structured Clinical Interview for DSM-IV-TR Axis I Disorders (First et al., 2002) to evaluate mental health status. None of the participants in the present study met diagnostic criteria for any mental health condition.

### 2.2. HLA Genotyping

DNA isolation was carried out from 3 ml of whole blood drawn in EDTA tubes, using a commercially available kit (ArchivePure cat. 2300730) from 5Prime (distributed by Fisher Scientific or VWR) with an expected yield of 50–150  $\mu$ g of DNA. The purified DNA samples were sent to Histogenetics (<http://www.histogenetics.com/>) for high-resolution HLA Sequence-based Typing (SBT; details are given in <https://bioinformatics.bethematchclinical.org/HLA-Resources/HLA-Typing/High-Resolution-Typing-Procedures/> and <https://bioinformatics.bethematchclinical.org/WorkArea/DownloadAsset.aspx?id=6482>). Their sequencing DNA templates are produced by locus- and group-specific amplifications that include exon 2 and 3 for class I (A, B, C) and exon 2 for class II (DRB1, DRB3/4/5, DQB1, and DPB1) and reported as Antigen Recognition Site (ARS) alleles as per ASHI recommendation (Cano et al., 2007).

### 2.3. MRI Data Acquisition and Preprocessing

All data were acquired using a Phillips 3T MR scanner (Achieva, Philips Healthcare, Best, The Netherlands). In the initial phase of the study, data were acquired from 42 participants using a phased array SENSitivity Encoding (SENSE) 8-channel head coil for reception. For each participant a high resolution T1-weighted Turbo Field Echo (T1w TFE SENSE) was obtained (168 sagittal slices, TR = 8.1932 ms, TE = 3.7520 ms, Acquisition matrix  $240 \times 240$ , Flip angle 8 deg., voxel size  $0.9375 \times 0.9375 \times 1$  mm). A T2-weighted image (T2w VISTA HR SENSE) was also obtained (180 slices, TR = 2500 ms, TE = 363.072 ms, Acquisition matrix  $252 \times 252$ , voxel size  $= 0.7813 \times 0.7813 \times 1$  mm). Subsequently, upgrades were applied to the system and data were acquired from the remainder 34 participants using a phased array SENSitivity Encoding (SENSE) 15-channel head coil for reception. For each participant a high resolution T1-weighted Turbo Field Echo (T1w TFE SENSE) was obtained (168 sagittal slices, TR = 8.0928 ms, TE = 3.698 ms, Acquisition matrix  $240 \times 240$ , Flip angle 8 deg., voxel size  $0.7500 \times 0.7500 \times 1$  mm). The T2-weighted (T2w VISTA HR SENSE) was also obtained (168 slices, TR = 2500 ms, TE = 370.346 ms, Acquisition matrix  $240 \times 240$ , voxel size  $= 0.7500 \times 0.7500 \times 1$  mm).

A 704-core High Performance Computing system (CentOS 6.5 Linux, Rocks 6.1.1) with Matlab R2012 (64 bit), Human Connectome Project (HCP [humanconnectome.org](http://humanconnectome.org)) pipeline with FreeSurfer (FS; <http://surfer.nmr.mgh.harvard.edu>) HCP version (freesurfer-hpc) was used for data processing. MRI data with high contrast between gray matter, white matter, and cerebrospinal fluid as well as high spatial resolution are necessary for accurate results. We acquired T1w and T2w images with high spatial resolution ( $\leq 1$  mm<sup>2</sup>) to achieve precise surface reconstruction. Standard FS software requires only T1w images as input. However, we used a modified version of FS, implemented in the structural HCP pipeline, which utilizes both T1w and T2w images to eliminate uncertainty due to the fact that dura and blood vessels are isointense to gray matter in the T1w image alone. In addition, T2w allows improved pial surface reconstruction (Glasser et al., 2013). Specifically, we used the first 2 structural HCP pipelines, namely *PreFreeSurfer* and *FreeSurfer*. One goal of the *PreFreeSurfer* pipeline is to align the T1w and T2w images. *PreFreeSurfer* pipeline processing was followed by *FreeSurfer* pipeline processing which is based on FS version 5.2 with improvements. From the segmentation statistics output we obtained estimated total intracranial volume (eTIV), and the volumes of left and right cerebellar gray matter, brainstem, thalamus, caudate, putamen, pallidum, accumbens, amygdala and diencephalon. We calculated the sum of the left and right volumes for each region and used them as dependent variables in the ANCOVA. Finally, the sum of these subcortical volumes was the “subcortical” brain volume.

### 2.4. Data Analysis

Standard statistical methods were employed to analyze the data using the IBM-SPSS statistical package (version 23). More specifically, we carried out a univariate and a multivariate analysis of covariance (ANCOVA) to assess the effect of DRB1\*13:02, DRB1\*13:01 and DRB1\*13 on brain volumes. In an initial analysis, we explored the possibility that the acquisition systems during the two phases of the study might have an effect on the results. For that purpose, we added a categorical “Acquisition” factor in the ANCOVAs, taking the values of 0 and 1 for the first and second phase of the study, respectively, and assessed its effect. In the univariate ANCOVA, the total subcortical volume was the dependent variable, the presence (or absence) of DRB1\*13:02 was a fixed factor, and sex, age, and eTIV were covariates. Since all carriers of this HLA allele were heterozygotes in our sample, the DRB1\*13:02 factor took values of zero and 1 in the ANCOVA. In repeated measures ANCOVAs, the Regions (N = 9 subcortical regions) were the Within-Subjects factor (since they came from the same subject), the presence

(or absence) of DRB1\*13:02 was the Between-Subjects factor, and sex, age, and eTIV were covariates. The same analyses were carried out for allele DRB1\*13:01.

## 3. Results

No participant carried both DRB1\*13:02 and DRB1\*13:01.

### 3.1. DRB1\*13:02

#### 3.1.1. Frequencies

Of the total of 76 participants, DRB1\*13:02 was present in 11 and absent in 65. The relative frequency of occurrence of this allele was  $\sim 7 \times$  higher in controls (8/21 = 0.38) than in GWI (3/55 = 0.054), indicating a protective effect of DRB1\*13:02 (Pearson chi-square = 13.08,  $P = 0.003$ ; estimated odds ratio ( $\hat{\omega}$ ) = 0.094,  $\ln(\hat{\omega}) = -2.367$ ,  $P = 0.001$ ) (Table 1).

#### 3.1.2. Volumes

The Acquisition factor did not have any statistically significant effect in any of the DRB1\*13:02-related ANCOVAs performed ( $P = 0.737$  for Acquisition Main Effect;  $P = 0.805$  for Acquisition X DRB1\*13:02 Interaction).

All statements on volumes below refer to volumes adjusted for sex, age and eTIV. Overall, mean volumes of the 9 subcortical regions (Table 2) were significantly higher in the presence than in the absence of DRB1\*13:02 ( $P = 0.028$ , Wilcoxon Signed Rank test). In addition, the overall subcortical volume (i.e. the sum of the volumes of all 9 subcortical regions) was significantly higher by 6.6% ( $P = 0.007$ , F-test in univariate ANCOVA) (Fig. 1). A more detailed analysis was carried out using a repeated measures ANCOVA (see Methods) which revealed that the effect of the Between-Subjects DRB1\*13:02 was highly significant ( $P = 0.007$ , F-test in repeated measures ANCOVA), as was the Region x DRB1\*13:02 interaction ( $P = 0.007$ , Greenhouse-Geisser test), reflecting the differential effect of DRB1\*13:02 on individual regions. Indeed, the strongest effect (9.6% higher in DRB1\*13:02) was observed in the cerebellar gray matter (Fig. 2).

### 3.2. DRB1\*13:01

#### 3.2.1. Frequencies

Of the total of 76 participants, DRB1\*13:01 was present in 10 and absent in 66. All DRB1\*13:01 carriers belonged to the GWI group. This higher frequency of occurrence of DRB1\*13:01 in GWI (18.2% vs zero) indicated an increased risk for GWI in carriers of DRB1\*13:01

**Table 1**

Results of two-way table analysis for DRB1\*13:02 and GWI.

A. Two-way table				
		Group Control	GWI	Total
DRB1*13:02	Absent	13	52	65
	Present	8	3	11
Total		21	55	76
B. Analysis of the two-way table				
Test	Value	DF	Significance (2-sided)	
Pearson Chi-Square	13.08	1	P = 0.0003	
C. Mantel-Haenszel common odds ratio estimate				
Estimated odds ratio ( $\hat{\omega}$ )	$\ln(\hat{\omega})$	SE of $\ln(\hat{\omega})$	Asymptotic significance (2-sided)	
0.094	-2.367	0.745	P = 0.001	
95% lower bound: 0.022				
95% upper bound: 0.403				



**Table 2**

Brain region volumes (mm<sup>3</sup>) (adjusted for sex, age, and eTIV) in the absence and presence of DRB1\*13:02.

Brain region	DRB1*13:02 Absent		DRB1*13:02 Present	
	Mean	SEM	Mean	SEM
Cerebellum Gray Matter <sup>a</sup>	78,116.5	1000.8	85,657.3	2497.6
Brainstem <sup>a</sup>	21,540.1	230.7	22,537.6	575.8
Thalamus <sup>a</sup>	14,198.0	160.4	14,554.4	400.3
Caudate <sup>a</sup>	7003.6	112.5	7411.2	280.8
Putamen <sup>a</sup>	9839.5	139.6	9811.5	348.4
Accumbens <sup>a</sup>	1088.4	19.5	1122.4	48.7
Pallidum <sup>a</sup>	2750.9	45.9	2851.1	114.7
Amygdala <sup>a</sup>	3278.0	49.1	3239.9	122.6
Diencephalon <sup>a</sup>	7421.6	80.2	7552.5	200.1
Total Subcortical <sup>b</sup>	145,236.5	1270.9	154,738.0	3171.7

<sup>a</sup> Statistics from a repeated measures ANCOVA where the 9 regions were the Within-Subjects factors, the absence or presence of DRB1\*13:02 was the Between-Subjects factor, and sex, age and eTIV were covariates.

<sup>b</sup> Statistics from a univariate ANCOVA where the subcortical volume was the dependent variable, the absence or presence of DRB1\*13:02 was a fixed factor, and sex, age and eTIV were covariates.

(Pearson chi-square = 4.397,  $P = 0.036$ ; estimated odds ratio ( $\hat{\omega}$ ) = 9.923,  $\ln(\hat{\omega}) = 2.29$ ) (Table 3).

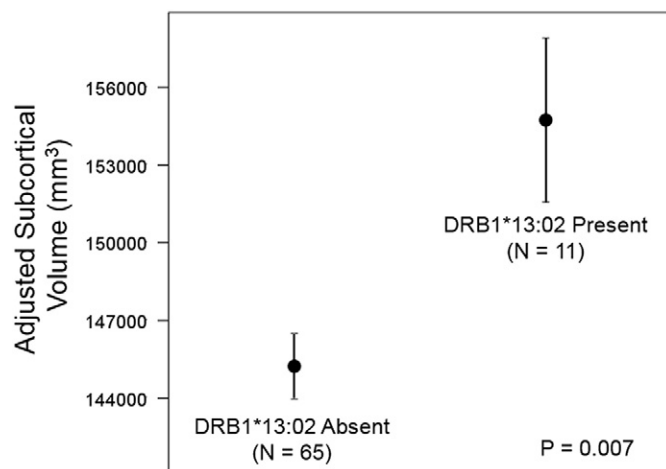
### 3.2.2. Volumes

The Acquisition factor did not have any statistically significant effect in any of the DRB1\*13:01-related ANCOVAs performed ( $P = 0.780$  for Acquisition Main Effect;  $P = 0.975$  for Acquisition X DRB1\*13:01 Interaction).

Overall, mean volumes of the 9 subcortical regions (adjusted for age, sex and eTIV) did not differ significantly between carriers and non-carriers of DRB1\*13:01 ( $P = 0.953$ , Wilcoxon Signed Rank test). The mean overall subcortical volume was 0.8% smaller in DRB1\*13:01 carriers but not significantly different ( $P = 0.756$ , F-test in univariate ANCOVA), and similarly for the volume of cerebellar gray matter (2.0% smaller in DRB1\*13:01 carriers;  $P = 0.592$ , F-test in univariate ANCOVA).

### 3.3. DRB1\*13

In this analysis, the fixed factor was the allele group DRB1\*13, which was deemed present when either DRB1\*13:01 or DRB1\*13:02 were present. No statistically significant results were yielded by any analysis.



**Fig. 1.** Mean ( $\pm$  SEM) subcortical volumes in the absence and presence of DRB1\*13:02. Statistics are from a univariate ANCOVA where the Subcortical volume was the dependent variables, the absence or presence of DRB1\*13:02 was a fixed factor, and sex, age and eTIV were covariates.

## 4. Discussion

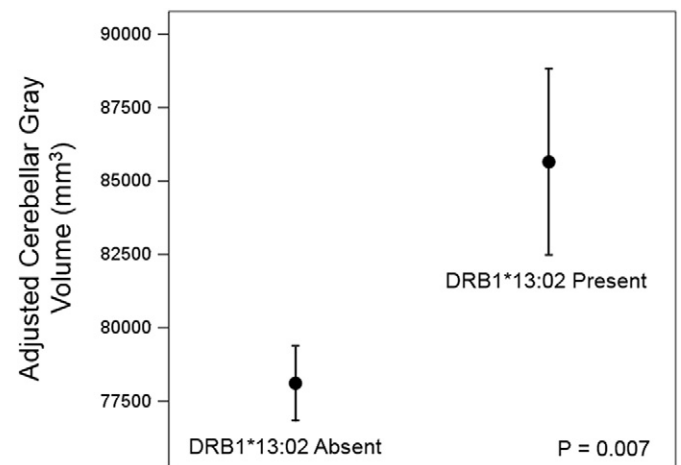
### 4.1. Protective Role of DRB1\*13:02

In this study we investigated possible protection conferred by HLA DRB1\*13:02 in GW veterans based on the facts that (a) DRB1\*13:02 is protective for GWI (Georgopoulos et al., 2016), (b) DRB1\*13:02 is broadly protective for immune-related disorders (Bettencourt et al., 2015; Furukawa et al., 2017; Hov et al., 2011), and (c) GWI is a neuroimmune disorder (James et al., 2016; Georgopoulos et al., 2017). Unlike typical studies based on analysis of relative frequencies of occurrence of DRB1\*13:02 in various healthy and disease populations (Bettencourt et al., 2015; Furukawa et al., 2017), we, additionally, assessed its effect on subcortical brain volumes found previously to be reduced in GWI (Christova et al., 2017); indeed, we found here that DRB1\*13:02 exerted a protective effect on these volumes and spared their atrophy. Specifically, the subcortical volume was significantly higher in carriers of DRB1\*13:02 than in non-carriers (Fig. 1); the strongest effect was observed in the cerebellar gray matter (Fig. 2). These findings are in keeping with the overall protective role of DRB1\*13:02 in immune-related disorders and in GWI, as reviewed above.

In contrast to DRB1\*13:02, DRB1\*13:01 had no significant effect on brain volumes in any analysis, although it was significantly more frequent in GWI. Although DRB1\*13:01 has been reported to have a protective role in various immune-related diseases (Furukawa et al., 2017), it has also been reported as risk factor for autoimmune hepatitis (Duarte-Rey et al., 2009) and primary sclerosing cholangitis (Hov et al., 2011).

### 4.2. The Importance of HLA-coded Proteins

Our findings above highlight the importance of working at the HLA-protein ( $\beta$ -chain) level, which is given by the 4-digit, high-resolution HLA genotyping, as advocated by Jones et al. (2006). Most studies of HLA-disease associations in general (too many to cite), have been focused at the gene level (e.g. DRB1, DQB1, etc.) or at the allele group level (e.g. DRB1\*01, DQB1\*02, etc.). However, the specificity of action of a HLA allele resides on the specific HLA protein ( $\beta$ -chain) coded by it, as specified by the second set of digits in the 4-digit resolution HLA genotyping (e.g. DRB1\*01:02, DPP1\*06:15, etc.). Given that different HLA proteins have different properties, it follows that the proper level of analysis is at this HLA-specific protein level. Looking for HLA-disease associations at the gene or allele group levels can be misleading,



**Fig. 2.** Mean ( $\pm$  SEM) volumes of cerebellar gray matter in the absence and presence of DRB1\*13:02. Statistics are from a multivariate ANCOVA where the cerebellar gray matter volume (one of 9 subcortical regions; see Table 2) was a dependent variable, the absence or presence of DRB1\*13:02 was a fixed factor, and sex, age and eTIV were covariates.

**Table 3**

Results of two-way table analysis for DRB1\*13:01 and GWI. The odds ratio was estimated after adding 0.5 to all counts to avoid taking the logarithm of zero. This procedure underestimates the true effect; statistics for the odds ratio cannot be calculated.

A. Two-way table				
		Group		Total
		Control	GWI	
DRB1*13:01	Absent	21	45	66
	Present	0	10	10
Total		21	55	76
B. Analysis of the two-way table				
Test	Value	DF	Significance (2-sided)	
Pearson Chi-Square	4.397	1	P = 0.036	
C. Mantel-Haenszel common odds ratio estimate				
Estimated odds ratio ( $\hat{\omega}$ )		$\ln(\hat{\omega})$		
9.923		2.295		

yielding mixed (risk/protective) or uncertain (i.e. statistically nonsignificant) results. This problem is compounded in studies of frequencies of occurrence of various HLA alleles in different populations (e.g. healthy or suffering from a specific disease) because of the large sample sizes needed and, therefore, the increased diversity expected of HLA-specific proteins in the sample. The findings of the present study illustrate these considerations clearly because the target of the study was a concrete biological variable (i.e. volume of a brain region) and not frequency of occurrence. This afforded a clear-cut evaluation of the effect of individual HLA proteins and a contrast between the effects of either HLA protein as well as the effect of the allele group DRB1\*13.

The importance of working at the HLA protein level was first demonstrated by Todd et al. (1987) in their pioneering study of the role of residue 57 of the HLA-DQ $\beta$  polypeptide in type 1 diabetes mellitus. Recent advances in HLA protein sequencing and 3-D conformation have opened new vistas in investigating HLA-disease relations (Brown et al., 1993; Jones et al., 2006). As succinctly expressed by Donaldson, “This changed the way in which HLA associations were perceived. No longer were they seen as unexplainable genetic anomalies; it was now possible to put these associations into a functional context.” (Donaldson, 2011, p 1798). Our study rests firmly on this approach. Actually, the study by Hov et al. (2011) on the relations between HLA proteins and primary sclerosing cholangitis (PSC) is directly relevant in discussing the results of our study. Hov et al. (2011) performed a 3-D modeling of the HLA-DR $\beta$  molecule to explore the effect of key residues on the 3-D configuration at the  $\beta$ -chain peptide binding groove. The charge of Pocket 9 (P9) of the peptide binding groove was differentially associated with PSC, such that a positive or negative charge is associated with PSC risk or protection, respectively. Specifically, Hov et al. (2011) found that in DRB1\*13:01 (a risk factor for PSC; Spurkland et al., 1999) a positive P9 charge was induced by a remote action of Valine at residue 86, whereas in DRB1\*13:02 (protective for PSC; Hov et al., 2011) a negative one was induced by glycine at that residue position. Extending the implications of this discovery to our study, it is reasonable to suppose that the sparing of subcortical brain atrophy we found to be associated with DRB1\*13:02 is due in part to the negative charge in P9, whereas a positive charge in P9 is neutral, since DRB1\*13:01 had no effect.

#### 4.3. The “Persistent Antigen” Hypothesis for GWI

All of the considerations above regarding the structural biological and physicochemical properties of the HLA-DR $\beta$  peptide binding groove ultimately relate to the family of external antigens that can bind to it, to be presented to CD4+ T lymphocytes for subsequent antibody production by B cells (Fig. 3). The ultimate goal of this HLA class II-mediated specific immunity is to eliminate pathogens by producing antibodies against them. The process of successful antibody production can be

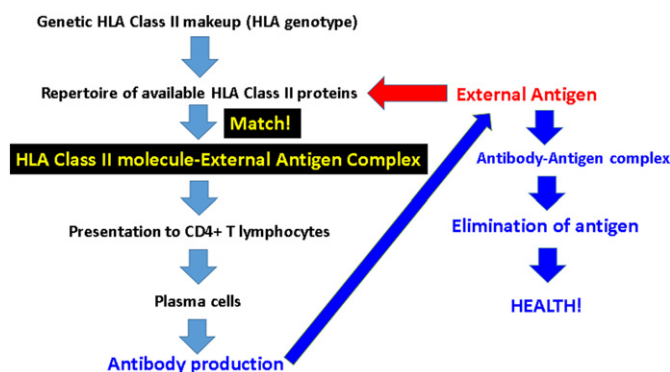


Fig. 3. Schematic diagram illustrating the steps of antibody production in health.

disrupted at different stages, from the absence of a match between antigen and HLA class II protein (due to genetic factors) to problems with CD4+ T cells and/or plasma cell function (due to disease and/or drugs) (Fig. 4). In such cases, the external antigen/pathogen is not eliminated and can persist in the body causing inflammation and ultimately cell damage, and potentially autoimmunity through molecular mimicry (Institute of Medicine, 2012). Assuming that GW veterans were healthy when activated (in 1990–91) with respect to lymphocyte function, and given that GWI is associated with genetic lack of HLA protection (Georgopoulos et al., 2016), the most likely scenario in GWI involves a lack of antigen match with HLA class II protein, resulting in persistent, pathogenic antigen, as illustrated in Fig. 4. We call this the “Persistent Antigen Hypothesis” for GWI. Although we do not know which specific pathogens were involved in GWI, an insight can be gained from the case of pediatric autoimmune hepatitis, for which DRB1\*13:01 is a risk (Fainboim et al., 2001) and DRB1\*13:02 a protective factor (Pando et al., 1999). Pediatric autoimmune hepatitis frequently follows a protracted course of infection with hepatitis A virus (Fainboim et al., 2001). These authors suggested that the protracted (but not acute) hepatitis A infection leads to a sustained release of liver self-antigens, which, in turn, lead to autoimmunity (Fainboim et al., 2001). Now, DRB1\*13:01 (but not DRB1\*13:02) was found to be strongly associated with the protracted forms of this infection and resulting autoimmune hepatitis. Thus a connection is made between a protracted, chronic infection and a developing autoimmune disease.

#### 4.4. Concluding Remarks

This line of evidence is in keeping with our “persistent antigen” hypothesis above for GWI pathogenesis. Such antigens could sustain low-grade inflammation and also lead to autoimmunity, both of which could underlie chronic inflammatory processes reported in GWI (Johnson et

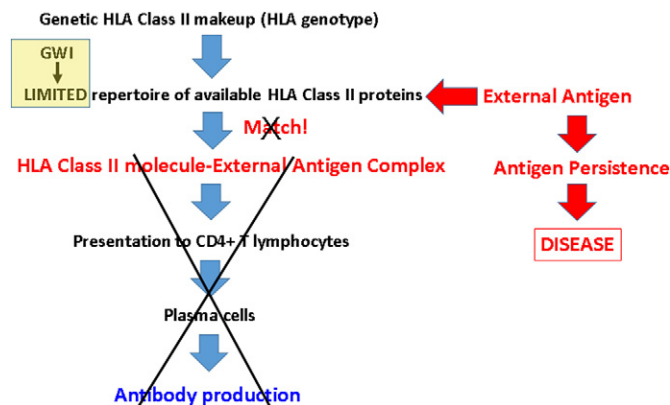


Fig. 4. Schematic diagram illustrating the disruption at various possible stages of antibody production leading to disease.

al., 2013). Either or both of these mechanisms (i.e. protracted low-grade inflammation and/or autoimmunity) could be involved in subcortical brain atrophy observed in GWI (Christova et al., 2017), as discussed in detail in that publication. Given the considerations above, it is possible that the protective role of DRB1\*13:02 may be primarily due to preventing infection by providing “matches” (Fig. 3) for many external antigens, leading to successful production of antibodies, eliminating pathogens and thus, in the long run, preventing autoimmunity. In other words, the DRB1\*13:02 protein would be a “pluripotent” HLA class II molecule. The reported protective role of DRB1\*13:02 against severe malaria (Hill et al., 1991) is in keeping with this notion.

Finally, a challenge for the future is the identification of persistent antigens in GWI and their elimination. Such antigens could come from the many antigens administered to GW veterans as vaccines (Institute of Medicine National Research Council, 2000, page 295) or from other exposures, and could be at the root of the involvement of several organs systems in GWI. If identified, they could be eliminated by administering specific antibodies, e.g. as an antiserum. These possibilities are currently under investigation in our laboratory.

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The authors do not report any financial disclosures.

### Author Contributions

Contributed to data collection and clinical evaluation: LMJ, PC, BEE, SML, AFC. Contributed to study design: APG, LMJ, PC, BEE, SML, AFC. Contributed to data analysis: LMJ, PC, APG. Wrote the paper: LMJ, APG. Contributed to editing the paper: All.

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# Gulf War illness (GWI) as a neuroimmune disease

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**Abstract** Gulf War illness (GWI) is a chronic disease characterized by the involvement of several organs, including the brain (Christova et al., Exp Brain Res doi:[10.1007/s00221-017-5010-8](https://doi.org/10.1007/s00221-017-5010-8), 2017). In a previous study (Georgopoulos et al., J Neural Eng 4:349–355, 2015), we identified six protective alleles from Class II human leukocyte antigen (HLA) genes, and more recently, we investigated the brain correlates of this protection (James et al., EBioMedicine 13:72–79, 2016). Those and other studies (Israeli, Lupus, 21:190–194, 2012) suggested an involvement of the immune system in GWI. In a recent study (Engdahl et al., EBioMedicine doi:[10.1016/j.ebiom.2016.08.030](https://doi.org/10.1016/j.ebiom.2016.08.030), 2016), we showed that the brain pattern of synchronous neural interactions (SNI; Georgopoulos et al., J Neural Eng 4:349–355, 2007) in GWI is distinctly different from that in healthy controls. Here we focused on

the SNI itself, as a basic measure of neural communication (irrespective of specific connections) and compared it between GWI and seven other diseases that cover a broad spectrum of etiology and pathophysiology. Specifically, we sought to determine which, if any, of those diseases might resemble GWI SNI, overall and within the HLA protective domain, and thus gain further knowledge regarding the nature of GWI brain abnormality. We studied a total of 962 participants from a healthy control population ( $N = 583$ ) and eight different diseases, including GWI ( $N = 40$ ), schizophrenia (SZ;  $N = 21$ ), Alzheimer's disease (AD;  $N = 66$ ), posttraumatic stress disorder (PTSD;  $N = 159$ ), major depressive disorder (MDD;  $N = 10$ ), relapsing–remitting multiple sclerosis (RRMS;  $N = 43$ ), Sjögren's syndrome (SS;  $N = 32$ ), and rheumatoid arthritis (RA;  $N = 8$ ). They all underwent a resting-state magnetoencephalographic (MEG) scan to calculate SNIs. Data were analyzed using analysis of covariance (ANCOVA) with disease as fixed factor, and sex and age as covariates. We found that GWI SNIs differed significantly from control SZ, AD, PTSD and MDD but not from RRMS, SS and RA. In addition, we compared GWI to RRMS, SS and RA with respect to SNIs of MEG sensor pairs that were related to the HLA alleles protective for GWI (James et al., EBioMedicine 13:72–79, 2016). We found that GWI SNIs did not differ significantly from any of these three diseases but they did so from control SZ, AD, PTSD and MDD. These findings indicate that (a) GWI brain synchronicity does not differ significantly from that of known immune-related diseases (RRMS, SS, RA), and (b) that this SNI similarity is present within the HLA-related SNIs. In contrast, GWI SNIs differed significantly from those of the other diseases. We conclude that altered brain communication in GWI likely reflects immune-related processes, as postulated previously (James et al., EBioMedicine 13:72–79, 2016). By extension, these findings also indicate

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that functional brain abnormalities in RRMS, SS and RA might be, in part, due to lack of protective HLA alleles as documented for GWI (Georgopoulos et al., *EBioMedicine* 3:79–85, 2015).

**Keywords** Gulf War illness (GWI) · Magnetoencephalography · Human leukocyte antigen (HLA) · Veterans · Schizophrenia · Alzheimer's disease · Posttraumatic stress disorder · Major depressive disorder · Relapsing–remitting multiple sclerosis · Sjögren's syndrome · Rheumatoid arthritis

## Introduction

### Gulf War illness (GWI)

Twenty-five years after the 1990–1991 Persian Gulf War, approximately 250,000 veterans continue to suffer from Gulf War illness (GWI), a condition characterized by chronic and diffuse physical and mental health symptoms that are not readily explained (White et al. 2016). Typical symptoms of GWI include widespread pain, fatigue, mood disruption, cognitive impairment and neurological abnormalities as well as skin rashes, respiratory complaints, and gastrointestinal problems (Fukuda et al. 1998; Steele 2000). The etiology of GWI remains unknown and definitive pathophysiological markers have not been identified. Recently, however, several lines of research suggest a clear explanation, specifically, that GWI involves immune system disruption (Georgopoulos et al. 2015; Parkitny et al. 2015; Skowera et al. 2004; Whistler et al. 2009) which is reflected (in part) in altered brain function (Engdahl et al. 2016; James et al. 2016) in genetically vulnerable individuals (Georgopoulos et al. 2015). Here we seek to extend that line of research and clarify GWI's relation to other immune-related conditions by comparing brain synchronicity in veterans with GWI to various immune- and non-immune-related diseases.

### Synchronous neural interactions (SNI)

Several magnetic resonance imaging studies have identified brain abnormalities associated with GWI (White et al. 2016), although various methodological differences have hampered identification of definitive GWI-related brain biomarkers. We have taken a different approach, focusing on SNIs derived from task-free magnetoencephalography (MEG). Healthy brain functioning is characterized by patterns of synchronized neural communications that are conserved across individuals (Langheim et al. 2006). In contrast, diseases involving the brain manifest characteristic aberrations in neural synchrony. To that end, we have demonstrated that SNIs successfully discriminate various

brain disorders including schizophrenia, chronic alcoholism, Sjögren's syndrome, multiple sclerosis, Alzheimer's disease temporomandibular joint disorder (Georgopoulos et al. 2007) and posttraumatic stress disorder (Georgopoulos et al. 2010; Engdahl et al. 2010) from each other and from healthy brain functioning. More recently, we demonstrated highly accurate discrimination of veterans with GWI from healthy controls based on regional SNI distributions (Engdahl et al. 2016), further substantiating the discriminatory power of SNI. In the current study, we compare SNI in GWI with that of healthy brain functioning and seven other diseases and to determine which, if any, resemble GWI.

## Rationale of the study

In the present study, we test our hypothesis that GWI is a neuroimmune disorder by comparing GWI SNI, irrespective of its regional brain distribution, to seven other diseases with neurological-cognitive-mood (NCM) symptoms of diverse etiology: schizophrenia, Alzheimer's disease, posttraumatic stress disorder, major depressive disorder, relapsing–remitting multiple sclerosis, Sjögren's syndrome, and rheumatoid arthritis. We hypothesized that GWI SNI would be similar to the latter three known immune-related diseases but not to the other conditions. Based on our prior work demonstrating HLA- and non-HLA-related brain effects on GWI symptoms (James et al. 2016), we also compared SNI across diseases with regard to HLA status.

## Materials and methods

### Study participants

A total of 962 human subjects participated in this study as paid volunteers. The study protocol was approved by the relevant institutional review boards and informed consent was obtained prior to the study. Exclusionary criteria included cardiac pacemakers or implanted ferrous metal, central nervous system disorders (e.g., Parkinson's disease, cerebrovascular accidents, a history of traumatic brain injury, etc.), and current alcohol or drug dependence. There were eight groups, including healthy controls (HC), patients with GWI, schizophrenia (SZ), Alzheimer's disease (AD), posttraumatic stress disorder (PTSD), major depressive disorder (MDD), relapsing–remitting multiple sclerosis (RRMS), Sjögren's syndrome (SS), and rheumatoid arthritis (RA). Demographic information (age and sex) and counts per group of zero-lag partial cross-correlations (synchronous neural interactions, SNI) are given in Table 1. The diagnoses for each patient group were made by a specialist in the respective field of medicine at the time of the study, as follows. GWI patients met both Centers for Disease Control

**Table 1** Demographic and SNI information for study groups

Group	Mean (years)	SD	N (participants)	N (men)	N (women)	N (SNI)	N (HLA-SNI)
Control	52.1	17.6	583	446	137	15531816	15012879
GW	50.0	7.7	40	36	4	997227	961726
SZ	45.0	9.4	21	17	4	537775	520457
AD	78.3	7.4	66	61	5	1600581	1556639
PTSD	50.9	14.8	159	139	20	4109160	3973161
MDD	50.5	11.9	10	9	1	193048	186546
RRMS	41.3	10.3	43	12	31	1195130	1148449
SS	55.3	11.0	32	4	28	867689	838534
RA	63.2	15.5	8	6	2	215331	206581

SD standard deviation, N counts, GW Gulf War illness, SZ schizophrenia, AD Alzheimer's disease, PTSD posttraumatic stress disorder, MDD major depressive disorder, RRMS relapsing–remitting multiple sclerosis, SS Sjögren's syndrome, RA rheumatoid arthritis

(Fukuda et al. 1998) and Kansas (Steele 2000) criteria. SZ patients were diagnosed based on DSM-IV criteria (APA 2000), had no history of electroconvulsive therapy, no past substance dependence, no current substance/alcohol dependence or abuse, and no medical conditions that effect the central nervous system (e.g., epilepsy). AD patients were diagnosed based on an interdisciplinary consensus diagnosis conference and determined to meet criteria for (1) a diagnosis of dementia according to DSM-IV (APA 2000) and (2) possible or probable AD according to NINCDS-ARDA criteria (McKhann et al. 1984). PTSD was diagnosed using the Clinician-Administered PTSD Scale for DSM-IV (CAPS; Blake et al. 1995). MDD was diagnosed using the Structured Clinical Interview for DSM-IV-TR Axis I Disorders (SCID; First et al. 2002). RRMS patients met the modified McDonald criteria (Polman et al. 2005), had greater than or equal to 10 T2 cerebral lesions, were at least 30 days post relapse or steroid burst, and had a clear relapsing–remitting MS subtype. SS patients were diagnosed based on the classification criteria by the American-European consensus group for Sjögren's syndrome (Vitali et al. 2002). They complained of cognitive dysfunction verified clinically by their physicians and by neuropsychological measurements. RA patients had their diagnosis established at the rheumatology clinic. Finally, the control group comprised age-matched subjects to the patient groups, as well as additional healthy subjects. Patients were receiving medications relevant to their brain illness; some of these medications were psychotropic.

### Data acquisition

All participants underwent a magnetoencephalographic (MEG) scan. As described previously (Georgopoulos et al. 2007, 2010), subjects lay supine within the electromagnetically shielded chamber and fixated their eyes on a spot ~65 cm in front of them, for 45–60 s. MEG data were acquired using a 248-channel axial gradiometer system

(Magne 3600WH, 4-D Neuroimaging, San Diego, CA), band-filtered between 0.1 and 400 Hz, and sampled at 1017.25 Hz. Data with artifacts (e.g., from non-removable metal or excessive subject motion) were eliminated from further analysis.

### Data analysis

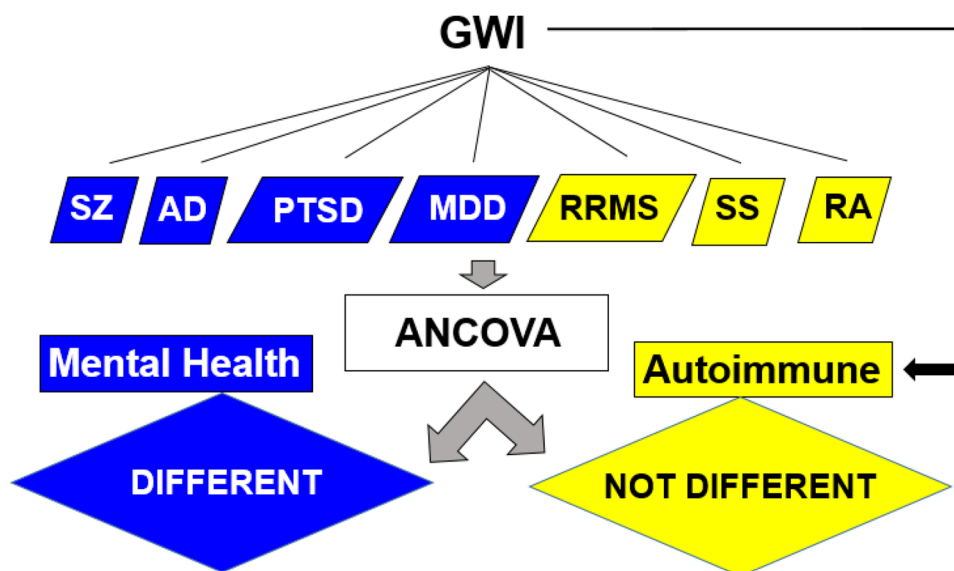
Standard statistical methods were used to analyze the data, including analysis of covariance (ANCOVA). The following packages were employed: IBM-SPSS statistical package, version 23, Matlab (version R2015b), and ad hoc Fortran computer programs employing the International Mathematics and Statistics Library (IMSL; Rogue Wave Software, Louisville, CO, USA) statistical and mathematical libraries. Prewhitening of the raw MEG series (see below) was performed using programs in Python (Mahan et al. 2015).

Single trial MEG time series from all sensors underwent 'prewhitening' (Box and Jenkins 1976; Priestley 1981) using a (50,1,3) ARIMA model (Mahan et al. 2015) to obtain innovations (i.e., residuals). All possible pairwise zero-lag cross-correlations ( $N = 30,628$ , given 248 sensors) were computed between the prewhitened MEG time series. Finally, the partial zero-lag cross-correlations  $PCC_{ij}^0$  (SNI) between  $i$  and  $j$  sensors were computed for all sensor pairs.  $PCC_{ij}^0$  was transformed to  $z_{ij}^0$  using Fisher's (Fisher 1958)  $z$  transformation to normalize its distribution:

$$SNI = z_{ij}^0 = \text{atanh}(PCC_{ij}^0) \quad (1)$$

An analysis of covariance (ANCOVA) was used to evaluate SNI differences between GWI and the remaining eight groups. For that purpose, SNIs were pooled from all subjects in each group; the number of SNIs per group are given in Table 1. Since age and sex differed among groups (Table 1), and since the objective was to test whether GWI SNIs differed significantly from those of the other groups, eight

**Fig. 1** Outline of study design and summary of outcomes of comparisons when all SNIs were used



ANCOVAs were carried out, one between GWI and each of the eight groups, where the SNI was the dependent variable, GWI and a specific disease were the Group fixed factor, and sex and age were covariates.

Additional analyses were performed to assess differences between GWI and other diseases in a subset of sensor pairs ( $N = 29219$ ) the SNIs of which were found previously to possess a significant relation to the presence of any one (or more) HLA alleles protective for GWI (James et al. 2016; Georgopoulos et al. 2015) with respect to NCM symptom severity. Therefore, eight additional ANCOVAs as above were performed for this HLA-related SNI subset.

## Results

### All sensor pairs (Fig. 1)

GWI SNIs differed significantly from those in the control group ( $P = 0.001$ ,  $F$  test in ANCOVA; Table 2). The results of the comparisons of GWI with the other seven disease groups are given in Table 2 and shown in Fig. 2. Of the seven diseases, GWI SNIs were highly significantly different from SZ, AD, PTSD, and MDD (the mental health disorders) but not so from RRMS, SS and RA, i.e., the three immune-related disorders.

### HLA-related sensor pairs

The location of sensors related to HLA protection (James et al. 2016) is shown in Fig. 3. HLA-related GWI SNIs (i.e., SNIs of all sensor pairs in Fig. 3) differed significantly from those in the control group ( $P < 0.001$ ,  $F$  test in ANCOVA; Table 3). The results of the comparisons of GWI with the

**Table 2** Results of ANCOVA comparing GWI to other diseases using all SNIs

Group	$F$	$df$ (denominator)	$P$ value
Control	10.686	16529039	0.001
SZ	62.968	1534998	$2.1 \times 10^{-15}$
AD	9.142	2597804	0.0025
PTSD	45.289	5106383	$1.7 \times 10^{-11}$
MDD	93.328	1190271	$4.4 \times 10^{-22}$
RRMS	2.157	2192353	0.142
SS	1.460	1864912	0.227
RA	1.707	1212554	0.191

Numerator  $F$  degrees of freedom = 1 for all ANCOVAs. Disease abbreviations are as in Table 1

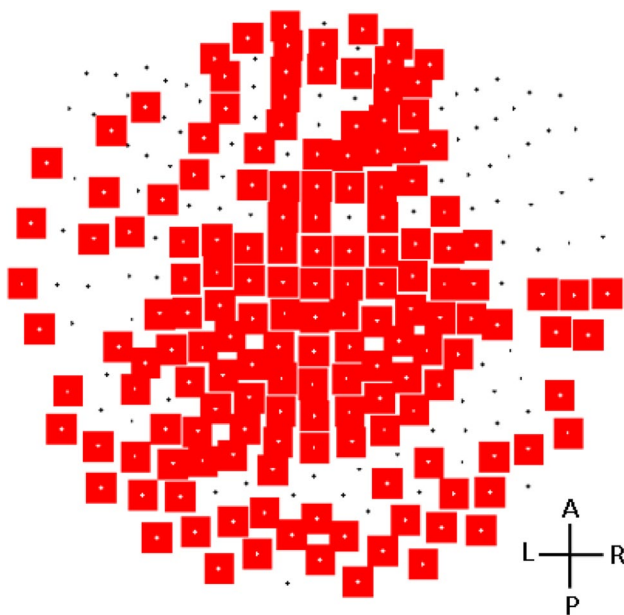
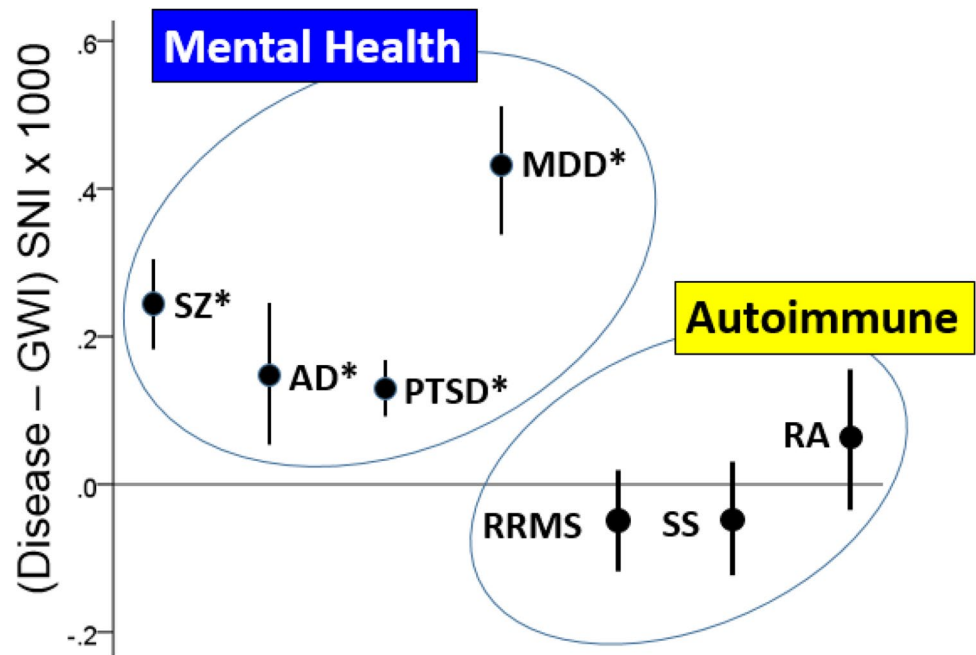
$F$   $F$  test for the Group factor in the ANCOVA,  $df$  degrees of freedom

other seven disease groups are given in Table 3 and shown in Fig. 4. Of the seven diseases, GWI SNIs were highly significantly different from SZ, AD, PTSD, and MDD (the mental health disorders) but not so from RRMS, SS and RA, i.e., the three immune-related disorders.

### Adjustment for multiple comparisons

The experimental design was for planned two-group comparisons (GWI vs. another group); the number of the ANCOVAs (=16 in total) reflected the number of groups compared (eight: GWI vs. control and seven disease groups)  $\times$  the two sets of sensor pairs (all and HLA-related). Thus, there were no multiple comparisons within each ANCOVA, and from this viewpoint, the probability values given in Tables 2 and 3 are valid at face value. However, it could be argued that an adjustment would be appropriate to account for the fact that 16 overall

**Fig. 2** Results for all sensor pairs to show means ( $\pm 2$ SEM) of SNI differences between stated disease group and GWI, adjusted for age and sex (ANCOVA). An asterisk denotes a statistically significant result, as detailed in Table 2



**Fig. 3** Territory of HLA-related SNIs. Red squares indicate the MEG sensors contributing to SNIs related to HLA, with respect to severity of NCM symptoms in GWI (James et al. 2016). A anterior; P posterior; L left; R right

comparisons were performed. For that purpose, we computed an adjusted  $P$  value using the Bonferroni correction. We found that for control SZ, AD, PTSD and MDD, all corrected values were  $P \leq 0.02$ , whereas for RRMS, SS and RA they were  $P = 1$ . Therefore, the essence of the results regarding the comparison of GWI SNIs against

**Table 3** Results of ANCOVA comparing GWI to other diseases using only HLA-related SNIs (see text)

Group	$F$	$df$ (denominator)	$P$ value
Control	18.351	15974601	0.000018
SZ	80.354	1482179	$3.1 \times 10^{-19}$
AD	11.203	2518361	0.001
PTSD	53.519	4934883	$2.6 \times 10^{-13}$
MDD	99.719	1148268	$1.8 \times 10^{-23}$
RRMS	0.141	2110175	0.707
SS	0.380	1800260	0.537
RA	1.551	1168303	0.213

Numerator  $F$  degrees of freedom = 1 for all ANCOVAs. Disease abbreviations are as in Table 1

$F$  test for the Group factor in the ANCOVA,  $df$  degrees of freedom

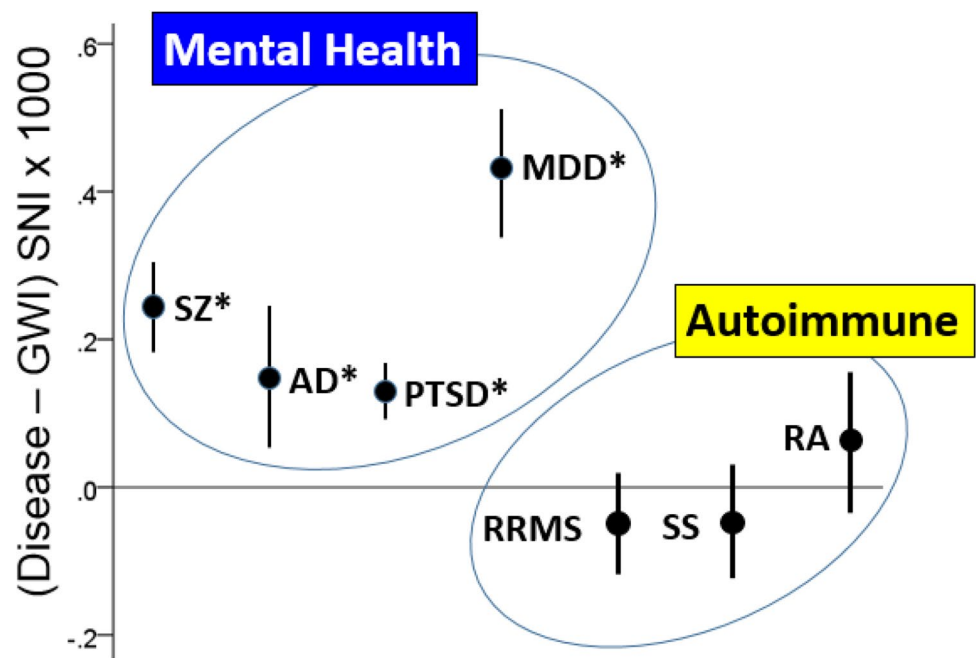
control, mental health disorders and immune-related disorders remains the same with or without Bonferroni correction.

## Discussion

### Neural synchronicity: SNI

In the present study, we evaluated brain synchronicity in GWI relative to seven other diseases and healthy brain functioning to test the hypothesis that GWI is a neuro-immune disease. For that purpose, we focused on the SNI itself, the basic measure of neural synchronicity,

**Fig. 4** Results for HLA-related sensor pairs to show means ( $\pm 2$ SEM) of SNI differences between stated disease group and GWI, adjusted for age and sex (ANCOVA). An *asterisk* denotes a statistically significant result, as detailed in Table 3



irrespective of its regional brain distribution. This approach complements our previous one that focused on differences of brain patterns of SNI (Georgopoulos et al. 2007, 2010; Engdahl et al. 2010, 2016). As expected, the results highlight similarities in brain synchronicity between GWI and known immune-related conditions and point to genetically mediated mechanisms underlying similarities between GWI and other immune-related diseases.

An asset of this study is the use of a fine-grain physiological measure of neural synchronicity (SNI) derived from high-fidelity (MEG) measurements to compare GWI with other diseases. SNIs (~30628/brain) come from a dense MEG sensor array (248 sensors) and cover most of the brain, thus providing a detailed background dataset on which comparisons are made. A reduction of this rich dataset to single values (e.g., mean SNI/brain) would eliminate all meaningful information and be, therefore, unwise. Indeed, use of individual SNIs as predictors has proved very innovative during the past 10 years in discriminating various diseases (Georgopoulos et al. 2007, 2010; James et al. 2014; Engdahl et al. 2016); in fact, it is on the basis of subsets of such single SNIs that classification of subjects to various diseases has been made. Finally, it could be argued that use of SNIs would tend to yield “significant” results due to the large number of degrees of freedom. However, the results of this study show that using SNIs did not just find or amplify “significant” effects: the outcomes (“significant” or “nonsignificant”) followed the nature of disease (immune-related or not) compared to GWI and did not just yield universally “significant” results.

A different issue concerns the neurobiological significance of neural synchronicity, which is measured by SNI. In general, neural synchronicity has been shown to be an important aspect of brain function in health and disease by many studies (see Singer 1999, and Uhlhaas and Singer 2006 for reviews). This is not surprising, since the essence of brain function as a massive communication network lies exactly in the interactions between neuronal populations. During the past decade, we have validated the clinical value of SNIs in several different ways. First, we showed that the brain pattern of SNI is very similar and robust across healthy subjects (Langheim et al. 2006). Second, we found that this pattern is distinctly different in brain disease, such as PTSD (Engdahl et al. 2010), GWI (Engdahl et al. 2016), and fetal alcohol syndrome (Lewis et al. 2016). Third, we showed that small subsets of SNIs can correctly classify with >90% accuracy healthy subjects and a number of brain diseases, including schizophrenia, Alzheimer’s disease, multiple sclerosis, Sjögren’s syndrome, temporomandibular joint disorder and chronic alcoholism (Georgopoulos et al. 2007), PTSD (Georgopoulos et al. 2010; James et al. 2014; Christova et al. 2015, using SNI from functional magnetic resonance data), and GWI (Engdahl et al. 2016). Finally, we have shown that neural synchronicity can be modulated in an orderly fashion by various, diverse factors, including trauma (James et al. 2012), pathological personality traits (James et al. 2015), posttraumatic growth (Anders et al. 2015), apolipoprotein E genotype (Leuthold et al. 2013), and HLA genes (James et al. 2016). Altogether, those studies have documented the importance of neural synchronicity as a fundamental aspect of brain network function and as an effective measure to



differentiate, quantify and evaluate the effects of disease and behavioral factors on integrative brain function.

### Immune basis of GWI

A number of researchers have implicated immune system disruption in GWI (Hotopf et al. 2000; Israeli 2012; Moss 2013; Parkitny et al. 2015; Skowera et al. 2004; Toubi 2012; Whistler et al. 2009). To that end, we recently demonstrated genetic vulnerability involving human leukocyte antigen (HLA) genes in veterans with GWI (Georgopoulos et al. 2015). HLA genes, which are located in the Major Histocompatibility Complex of chromosome 6, play a central role in immune system functioning (Meuer et al. 1982). We reported that six Class II HLA alleles discriminate veterans with GWI from healthy controls and are inversely related to GWI symptom severity, suggesting a protective effect (Georgopoulos et al. 2015). That is, veterans with GWI lack protection, thereby increasing the likelihood of immune-related reactions and other aberrant immune responses when exposed to environmental triggers. We also demonstrated that these HLA alleles interact with brain function to influence symptoms of GWI including NCM (James et al. 2016). There, we concluded that in the absence of HLA protection, immune-related brain abnormalities develop in GWI, perhaps via the development of antibodies to brain antigens resulting in cellular abnormalities, anomalies in neural communication, and symptomatology.

### Brain dysfunction in GWI and other disorders with immune involvement

GWI is associated with structural brain abnormalities, notably subcortical brain atrophy (Christova et al. 2017). Functionally, more than half of veterans with GWI report at least moderate neurological/cognitive/mood (NCM) impairment (Steele 2000). Typical symptoms include memory and concentration difficulty, word-finding trouble, headaches, blurred vision, tremors, numbness, and mood alterations among others. Similar cognitive and neuropsychiatric symptoms have been associated with various conditions characterized by disruptions in immune functioning including rheumatoid arthritis (Hanly et al. 2005; Shin et al. 2012, 2013; de Melo and Da-Silva 2012), systemic lupus erythematosus (Ainala et al. 2001; Antonchak et al. 2011; Carbotte et al. 1986; de Melo and Da-Silva 2012; Ginsburg et al. 1992; Hanly et al. 1994, 2005; Hay et al. 1992) Sjögren's syndrome (Alexander and Provost 1987; Lafitte et al. 2001; Martinez et al. 2010; Segal et al. 2012, 2014), and multiple sclerosis (Amato et al. 2006; Chiaravalloti and DeLuca 2008; Denney et al. 2005; Rao et al. 1991). Although estimates vary, some studies have found that two thirds of patients with these disorders exhibit

cognitive impairment (Ainala et al. 2001; Hamed et al. 2012; Carbotte et al. 1986; Alexander and Provost 1987; Heaton et al. 1985). These deficits are observed in individuals with no prior cognitive or psychiatric history and have been shown to be associated with markers of inflammation or autoimmunity (Alexander and Provost 1987; Kozora et al. 2001; Hamed et al. 2012). Thus, like GWI, these conditions appear to exhibit interacting effects on the nervous system and immune system that result in both NCM impairment and immune system disruption.

### GWI SNI differences from other diseases

We have previously demonstrated the power of SNI brain patterns derived from task-free MEG in successfully discriminating various brain diseases (Georgopoulos et al. 2007, 2010; Engdahl et al. 2010, 2016; James et al. 2014). In the present study, we compared average GWI SNI, irrespective of its brain distribution, to healthy brain functioning and other diseases of varied etiology, all of which involve NCM-related impairments. Results demonstrated that GWI SNI did not differ significantly from that of three immune-related diseases (SS, RRMS, and RA) but differed significantly from healthy brain functioning and from brain functioning in non-immune-related diseases (SZ, AD, PTSD, MDD), supporting our hypothesis that GWI is a neuroimmune disease. Although many researchers have recently surmised that GWI is an immune-related condition, this is the first study to empirically demonstrate brain-related similarities between GWI and known immune diseases.

### GWI differences within protective HLA-related SNIs

In previous studies, we demonstrated HLA-involvement in GWI (Georgopoulos et al. 2015) as well as HLA-related neural influences on GWI symptoms (James et al. 2016). Here we sought to further evaluate SNI differences between GWI and the three immune-related diseases with regard to HLA status. The vast majority of SNIs (29219 out of 30628) were significantly related to HLA with respect to GWI NCM severity (James et al. 2016), highlighting robust interactions of neural and immune systems in GWI. The SNIs involved were widespread although entirely absent in the right temporal region (Fig. 3) and sparse in the right temporal region. Within this subset of HLA-related SNIs, there were no significant differences between GWI and the three immune-related diseases: RA, RRMS, and SS, in contrast to significant differences present between GWI and the four non-immune-related diseases (SZ, AD, PTSD, MDD).

## Implications for possible HLA protective involvement in other diseases

The results of the present study highlight neuroimmune involvement in GWI and indicate brain-based similarities with other immune disorders, particularly with regard to HLA-related neural synchrony. Here, the focus is on disease and, with regard to HLA-related SNI, GWI is indistinguishable from RRMS, RA, and SS. However, in as much as the absence of certain HLA alleles has been linked to enhanced vulnerability for GWI, the presence of those alleles confers protection (Georgopoulos et al. 2015). This suggests the possibility that these same alleles may confer protection for brain involvement in other neuroimmune diseases as well. Interestingly, DRB1\*13:02, one of our six GWI protective alleles (Georgopoulos et al. 2015), has been found to confer protection to a wide variety of immune-related disorders (Furukawa et al. 2017). This adds further support to the link between GWI and lack of HLA protection (Georgopoulos et al. 2015).

## Limitation of the study

The main limitation of the study is the relatively small number of participants in the disease groups. Although the number of SNIs was large and allowed valid comparisons, the representation of adequate variety across participants with various diseases is important. Another possible limitation concerns the criteria used for diagnosis. In the present study, disease diagnosis was made by expert clinician at the time of study but such criteria may change over time. This limitation holds for many clinical studies and trials.

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## Compliance with ethical standards

**Conflict of interest** The authors do not report any financial disclosures or conflicts of interest.

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